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RAW SEQUENCE LISTING

DATE: 07/09/2002

PATENT APPLICATION: US/10/026,021

TIME: 16:20:42

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3 <110> APPLICANT: Hitoshi, Yasumichi
4      Demo, Susan
5      Jenkins, Yonchu
6      Rigel Pharmaceuticals, Inc.
8 <120> TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
9      Treatment of Cancer
11 <130> FILE REFERENCE: 021044-001210US
13 <140> CURRENT APPLICATION NUMBER: US 10/026,021
C--> 14 <141> CURRENT FILING DATE: 2002-06-25
16 <150> PRIOR APPLICATION NUMBER: US 60/309,632
17 <151> PRIOR FILING DATE: 2001-08-01
19 <160> NUMBER OF SEQ ID NOS: 8
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
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25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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30 <222> LOCATION: (1)..(2913)
31 <223> OTHER INFORMATION: human SAK serine/threonine kinase
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36 1          5          10          15
38 ctg ctt ggt aaa gga tca ttt gct ggt gtc tac aga gct gag tcc att      96
39 Leu Leu Gly Lys Gly Ser Phe Ala Gly Val Tyr Arg Ala Glu Ser Ile
40          20          25          30
42 cac act ggt ttg gaa gtt gca atc aaa atg ata gat aag aaa gcc atg      144
43 His Thr Gly Leu Glu Val Ala Ile Lys Met Ile Asp Lys Lys Ala Met
44          35          40          45
46 tac aaa gca gga atg gta cag aga gtc caa aat gag gtg aaa ata cat      192
47 Tyr Lys Ala Gly Met Val Gln Arg Val Gln Asn Glu Val Lys Ile His
48          50          55          60
50 tgc caa ttg aaa cat cct tct atc ttg gag ctt tat aac tat ttt gaa      240
51 Cys Gln Leu Lys His Pro Ser Ile Leu Glu Leu Tyr Asn Tyr Phe Glu
52 65          70          75          80
54 gat agc aat tat gtg tat ctg gta tta gaa atg tgc cat aat gga gaa      288
55 Asp Ser Asn Tyr Val Tyr Leu Val Leu Glu Met Cys His Asn Gly Glu
56          85          90          95
58 atg aac agg tat cta aag aat aga gtg aaa ccc ttc tca gaa aat gaa      336
59 Met Asn Arg Tyr Leu Lys Asn Arg Val Lys Pro Phe Ser Glu Asn Glu
60          100          105          110

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62 gct cga cac ttc atg cac cag atc atc aca ggg atg ttg tat ctt cat 384
63 Ala Arg His Phe Met His Gln Ile Ile Thr Gly Met Leu Tyr Leu His
64      115      120      125
66 tct cat ggt ata cta cac cgg gac ctc aca ctt tct aac ctc cta ctg 432
67 Ser His Gly Ile Leu His Arg Asp Leu Thr Leu Ser Asn Leu Leu Leu
68      130      135      140
70 act cgt aat atg aac atc aag att gct gat ttt ggg ctg gca act caa 480
71 Thr Arg Asn Met Asn Ile Lys Ile Ala Asp Phe Gly Leu Ala Thr Gln
72 145      150      155      160
74 ctg aaa atg cca cat gaa aag cac tat aca tta tgt gga act cct aac 528
75 Leu Lys Met Pro His Glu Lys His Tyr Thr Leu Cys Gly Thr Pro Asn
76      165      170      175
78 tac att tca cca gaa att gcc act cga agt gca cat ggc ctt gaa tct 576
79 Tyr Ile Ser Pro Glu Ile Ala Thr Arg Ser Ala His Gly Leu Glu Ser
80      180      185      190
82 gat gtt tgg tcc ctg ggc tgt atg ttt tat aca tta ctt atc ggg aga 624
83 Asp Val Trp Ser Leu Gly Cys Met Phe Tyr Thr Leu Leu Ile Gly Arg
84      195      200      205
86 cca ccc ttc gac act gac aca gtc aag aac aca tta aat aaa gta gta 672
87 Pro Pro Phe Asp Thr Asp Thr Val Lys Asn Thr Leu Asn Lys Val Val
88      210      215      220
90 ttg gca gat tat gaa atg cca tct ttt ttg tca ata gag gcc aag gac 720
91 Leu Ala Asp Tyr Glu Met Pro Ser Phe Leu Ser Ile Glu Ala Lys Asp
92 225      230      235      240
94 ctt att cac cag tta ctt cgt aga aat cca gca gat cgt tta agt ctg 768
95 Leu Ile His Gln Leu Leu Arg Arg Asn Pro Ala Asp Arg Leu Ser Leu
96      245      250      255
98 tct tca gta ttg gac cat cct ttt atg tcc cga aat tct tca aca aaa 816
99 Ser Ser Val Leu Asp His Pro Phe Met Ser Arg Asn Ser Ser Thr Lys
100      260      265      270
102 agt aaa gat tta gga act gtg gaa gac tca att gat agt ggg cat gcc 864
103 Ser Lys Asp Leu Gly Thr Val Glu Asp Ser Ile Asp Ser Gly His Ala
104      275      280      285
106 aca att tct act gca att aca gct tct tcc agt acc agt ata agt ggt 912
107 Thr Ile Ser Thr Ala Ile Thr Ala Ser Ser Ser Thr Ser Ile Ser Gly
108      290      295      300
110 agt tta ttt gac aaa aga aga ctt ttg att ggt cag cca ctc cca aat 960
111 Ser Leu Phe Asp Lys Arg Arg Leu Leu Ile Gly Gln Pro Leu Pro Asn
112 305      310      315      320
114 aaa atg act gta ttt cca aag aat aaa agt tca act gat ttt tct tct 1008
115 Lys Met Thr Val Phe Pro Lys Asn Lys Ser Ser Thr Asp Phe Ser Ser
116      325      330      335
118 tca gga gat gga aac agt ttt tat act cag tgg gga aat caa gaa acc 1056
119 Ser Gly Asp Gly Asn Ser Phe Tyr Thr Gln Trp Gly Asn Gln Glu Thr
120      340      345      350
122 agt aat agt gga agg gga aga gta att caa gat gca gaa gaa agg cca 1104
123 Ser Asn Ser Gly Arg Gly Arg Val Ile Gln Asp Ala Glu Glu Arg Pro
124      355      360      365
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131	Ser	Asn	Ser	Gln	Ser	Gln	Ala	Lys	Thr	Tyr	Thr	Met	Glu	Arg	Cys	His	
132	385					390					395				400		
134	tca	gca	gaa	atg	ctt	tca	gtg	tcc	aaa	aga	tca	gga	gga	ggt	gaa	aat	1248
135	Ser	Ala	Glu	Met	Leu	Ser	Val	Ser	Lys	Arg	Ser	Gly	Gly	Gly	Glu	Asn	
136					405					410					415		
138	gaa	gag	agg	tac	tca	ccc	aca	gac	aac	aat	gcc	aac	att	ttt	aac	ttc	1296
139	Glu	Glu	Arg	Tyr	Ser	Pro	Thr	Asp	Asn	Asn	Ala	Asn	Ile	Phe	Asn	Phe	
140				420					425					430			
142	ttt	aaa	gaa	aag	aca	tcc	agt	agt	tct	gga	tct	ttt	gaa	aga	cct	gat	1344
143	Phe	Lys	Glu	Lys	Thr	Ser	Ser	Ser	Ser	Gly	Ser	Phe	Glu	Arg	Pro	Asp	
144		435					440					445					
146	aac	aat	caa	gca	ctc	tcc	aat	cat	ctt	tgt	cca	gga	aaa	act	cct	ttt	1392
147	Asn	Asn	Gln	Ala	Leu	Ser	Asn	His	Leu	Cys	Pro	Gly	Lys	Thr	Pro	Phe	
148		450					455					460					
150	cca	ttt	gca	gac	cag	aca	cct	cag	act	gaa	acc	gta	caa	cag	tgg	ttt	1440
151	Pro	Phe	Ala	Asp	Pro	Thr	Pro	Gln	Thr	Glu	Thr	Val	Gln	Gln	Trp	Phe	
152	465				470					475					480		
154	ggg	aat	ctg	caa	ata	aat	gct	cat	tta	aga	aaa	act	act	gaa	tat	gac	1488
155	Gly	Asn	Leu	Gln	Ile	Asn	Ala	His	Leu	Arg	Lys	Thr	Thr	Glu	Tyr	Asp	
156				485					490					495			
158	agc	atc	agc	cca	aac	cgg	gac	ttc	cag	ggc	cat	cca	gat	ttg	cag	aag	1536
159	Ser	Ile	Ser	Pro	Asn	Arg	Asp	Phe	Gln	Gly	His	Pro	Asp	Leu	Gln	Lys	
160				500					505					510			
162	gac	aca	tca	aaa	aat	gcc	tgg	act	gat	aca	aaa	gtc	aaa	aag	aac	tct	1584
163	Asp	Thr	Ser	Lys	Asn	Ala	Trp	Thr	Asp	Thr	Lys	Val	Lys	Lys	Asn	Ser	
164			515					520				525					
166	gat	gct	tct	gat	aat	gca	cat	tct	gta	aaa	cag	caa	aat	acc	atg	aaa	1632
167	Asp	Ala	Ser	Asp	Asn	Ala	His	Ser	Val	Lys	Gln	Gln	Asn	Thr	Met	Lys	
168		530				535					540						
170	tat	atg	act	gca	ctt	cac	agt	aaa	cct	gag	ata	atc	caa	caa	gaa	tgt	1680
171	Tyr	Met	Thr	Ala	Leu	His	Ser	Lys	Pro	Glu	Ile	Ile	Gln	Gln	Glu	Cys	
172	545				550					555					560		
174	gtt	ttt	ggc	tca	gat	cct	ctt	tct	gaa	cag	agc	aag	act	agg	ggt	atg	1728
175	Val	Phe	Gly	Ser	Asp	Pro	Leu	Ser	Glu	Gln	Ser	Lys	Thr	Arg	Gly	Met	
176				565					570					575			
178	gag	cca	cca	tgg	ggt	tat	cag	aat	cgt	aca	tta	aga	agc	att	aca	tct	1776
179	Glu	Pro	Pro	Trp	Gly	Tyr	Gln	Asn	Arg	Thr	Leu	Arg	Ser	Ile	Thr	Ser	
180				580					585					590			
182	ccg	ttg	gtt	gct	cac	agg	tta	aaa	cca	atc	aga	cag	aaa	acc	aaa	aag	1824
183	Pro	Leu	Val	Ala	His	Arg	Leu	Lys	Pro	Ile	Arg	Gln	Lys	Thr	Lys	Lys	
184			595				600					605					
186	gct	gtg	gtg	agc	ata	ctt	gat	tca	gag	gag	gtg	tgt	gtg	gag	ctt	gta	1872
187	Ala	Val	Val	Ser	Ile	Leu	Asp	Ser	Glu	Glu	Val	Cys	Val	Glu	Leu	Val	
188		610				615					620						
190	aag	gag	tat	gca	tct	caa	gaa	tat	gtg	aaa	gaa	gtt	ctt	cag	ata	tct	1920
191	Lys	Glu	Tyr	Ala	Ser	Gln	Glu	Tyr	Val	Lys	Glu	Val	Leu	Gln	Ile	Ser	

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196			645		650		655	
198	ttt cct ctt gct gat aga cca ccc tca cct act gac aac atc agt agg	2016						
199	Phe Pro Leu Ala Asp Arg Pro Pro Ser Pro Thr Asp Asn Ile Ser Arg							
200			660		665		670	
202	tac agc ttt gac aat tta cca gaa aaa tac tgg cga aaa tat caa tat	2064						
203	Tyr Ser Phe Asp Asn Leu Pro Glu Lys Tyr Trp Arg Lys Tyr Gln Tyr							
204			675		680		685	
206	gct tcc agg ttt gta cag ctt gta aga tct aaa tct ccc aaa atc act	2112						
207	Ala Ser Arg Phe Val Gln Leu Val Arg Ser Lys Ser Pro Lys Ile Thr							
208			690		695		700	
210	tat ttt aca aga tat gct aaa tgc att ttg atg gag aat tct cct ggt	2160						
211	Tyr Phe Thr Arg Tyr Ala Lys Cys Ile Leu Met Glu Asn Ser Pro Gly							
212	705		710		715		720	
214	gct gat ttt gag gtt tgg ttt tat gat ggg gta aaa ata cac aaa aca	2208						
215	Ala Asp Phe Glu Val Trp Phe Tyr Asp Gly Val Lys Ile His Lys Thr							
216			725		730		735	
218	gaa gat ttc att cag gtg att gaa aag aca ggg aag tct tac act tta	2256						
219	Glu Asp Phe Ile Gln Val Ile Glu Lys Thr Gly Lys Ser Tyr Thr Leu							
220			740		745		750	
222	aaa agt gaa agt gaa gtt aat agc ttg aaa gag gag ata aaa atg tat	2304						
223	Lys Ser Glu Ser Glu Val Asn Ser Leu Lys Glu Glu Ile Lys Met Tyr							
224			755		760		765	
226	atg gac cat gct aat gag ggt cat cgt att tgt tta gca ctg gaa tcc	2352						
227	Met Asp His Ala Asn Glu Gly His Arg Ile Cys Leu Ala Leu Glu Ser							
228			770		775		780	
230	ata att tca gaa gag gaa agg aaa act agg agt gct ccc ttt ttc cca	2400						
231	Ile Ile Ser Glu Glu Glu Arg Lys Thr Arg Ser Ala Pro Phe Phe Pro							
232	785		790		795		800	
234	ata atc ata gga aga aaa cct ggt agt act agt tca cct aag gcc tta	2448						
235	Ile Ile Ile Gly Arg Lys Pro Gly Ser Thr Ser Ser Pro Lys Ala Leu							
236			805		810		815	
238	tca cct cct cct tct gtg gat tca aat tac cca acg aga gat aga gca	2496						
239	Ser Pro Pro Pro Ser Val Asp Ser Asn Tyr Pro Thr Arg Asp Arg Ala							
240			820		825		830	
242	tct ttc aac aga atg gtc atg cat agt gct gct tct cca aca cag gca	2544						
243	Ser Phe Asn Arg Met Val Met His Ser Ala Ala Ser Pro Thr Gln Ala							
244			835		840		845	
246	cca atc ctt aat ccc tct atg gtt aca aat gaa gga ctt ggt ctt aca	2592						
247	Pro Ile Leu Asn Pro Ser Met Val Thr Asn Glu Gly Leu Gly Leu Thr							
248			850		855		860	
250	act aca gct tct gga aca gac atc tct tct aat agt cta aaa gat tgt	2640						
251	Thr Thr Ala Ser Gly Thr Asp Ile Ser Ser Asn Ser Leu Lys Asp Cys							
252	865		870		875		880	
254	ctt cct aaa tca gca caa ctt ttg aaa tct gtt ttt gtg aaa aat gtt	2688						
255	Leu Pro Lys Ser Ala Gln Leu Leu Lys Ser Val Phe Val Lys Asn Val							
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262 gat ggg tcc cag ttg gtt gtg cag gca gga gtg tct tct atc agt tat 2784
263 Asp Gly Ser Gln Leu Val Val Gln Ala Gly Val Ser Ser Ile Ser Tyr
264          915          920          925
266 acc tca cca aat ggt caa aca act agg tat gga gaa aat gaa aaa tta 2832
267 Thr Ser Pro Asn Gly Gln Thr Thr Arg Tyr Gly Glu Asn Glu Lys Leu
268          930          935          940
270 cca gac tac atc aaa cag aaa tta cag tgt ctg tct tcc atc ctt ttg 2880
271 Pro Asp Tyr Ile Lys Gln Lys Leu Gln Cys Leu Ser Ser Ile Leu Leu
272 945          950          955          960
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293 35 40 45
294 Tyr Lys Ala Gly Met Val Gln Arg Val Gln Asn Glu Val Lys Ile His
295 50 55 60
296 Cys Gln Leu Lys His Pro Ser Ile Leu Glu Leu Tyr Asn Tyr Phe Glu
297 65 70 75 80
298 Asp Ser Asn Tyr Val Tyr Leu Val Leu Glu Met Cys His Asn Gly Glu
299 85 90 95
300 Met Asn Arg Tyr Leu Lys Asn Arg Val Lys Pro Phe Ser Glu Asn Glu
301 100 105 110
302 Ala Arg His Phe Met His Gln Ile Ile Thr Gly Met Leu Tyr Leu His
303 115 120 125
304 Ser His Gly Ile Leu His Arg Asp Leu Thr Leu Ser Asn Leu Leu Leu
305 130 135 140
306 Thr Arg Asn Met Asn Ile Lys Ile Ala Asp Phe Gly Leu Ala Thr Gln
307 145 150 155 160
308 Leu Lys Met Pro His Glu Lys His Tyr Thr Leu Cys Gly Thr Pro Asn
309 165 170 175
310 Tyr Ile Ser Pro Glu Ile Ala Thr Arg Ser Ala His Gly Leu Glu Ser
311 180 185 190
312 Asp Val Trp Ser Leu Gly Cys Met Phe Tyr Thr Leu Leu Ile Gly Arg
313 195 200 205
314 Pro Pro Phe Asp Thr Asp Thr Val Lys Asn Thr Leu Asn Lys Val Val

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VERIFICATION SUMMARY

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